



Serial No.: 08/984,099
Group Art Unit: 1638

Pending Claims

Sb > *J*
F1

(FIVE TIMES AMENDED)

1. A DNA sequence comprising as operably joined components in the direction of transcription, a cotton fiber transcriptional initiation region functional in a cotton fiber cell and an open reading frame encoding a protein in a pigment biosynthesis pathway, wherein said transcriptional initiation region is selected from the group consisting of:
 - a. nucleotides 65-4163 of SEQ ID NO: 7, and
 - b. SEQ ID NO: 15.

- F2*
- (AMENDED)
2. The DNA sequence according to Claim 1, further comprising a sequence encoding a transit peptide from a plant nuclear-encoded gene.

- F3*
- (TWICE AMENDED)
3. The DNA sequence according to Claim 2, wherein said transit peptide is a plastid transit peptide.

- Sb* > *G*
- (TWICE AMENDED)
4. The DNA sequence according to Claim 1, wherein said DNA sequence further comprises as an operably joined component a sequence encoding a transit peptide from a signal peptide which provides for transport across the rough endoplasmic reticulum.

- F4*
- (AMENDED)
5. The DNA sequence according to Claim 4, wherein said DNA sequence further comprises as an operably joined component, 3' to said open reading frame, a sequence encoding a vacuolar targeting signal.

6. The DNA sequence of Claim 1 wherein said pigment is melanin or indigo.
7. The DNA sequence of Claim 1 wherein said open reading frame is from a bacterial or a plant gene.
8. The DNA sequence of Claim 7 wherein said gene is selected from the group consisting of ORF438, tyrA, anthocyanin R gene, anthocyanin C1 gene, pig, and tna.

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9. A DNA construct comprising a DNA sequence of Claim 1.

Sub G12 F5
~~(TWICE AMENDED)~~
10. A DNA construct comprising a first and a second DNA sequence according to Claim 1, wherein the open reading frame of said first DNA sequence encodes a different gene than the open reading frame of said second DNA sequence.

Sub G13 F6
~~36 (AMENDED) 28~~
12. A plant cell comprising the DNA construct of Claim 9.

Sub G13 F6
~~37 (AMENDED) 36~~
13. A plant comprising the cell of Claim 12.

Sub G13 F7
~~(THREE TIMES AMENDED)~~
14. A method of modifying fiber phenotype in a cotton plant, said method comprising: transforming a plant cell with the DNA construct according to Claim 9 or 10; and regenerating a plant comprising fiber tissue from said plant cell, wherein said fiber tissue comprises a substrate of said protein in a pigment biosynthesis pathway, and wherein said protein reacts with said substrate to produce said pigment, whereby the phenotype of said fiber is modified.

Sub G13 F8
~~41 (TWICE AMENDED) 40~~
15. The method of Claim 14 wherein said DNA construct further comprises a sequence encoding a transit peptide from a plant nuclear-encoded gene.

Sub G13 F9
~~(TWICE AMENDED)~~
16. The method of Claim 14 wherein said DNA construct further comprises a sequence encoding a transit peptide, which encodes a signal peptide which provides for transport across the rough endoplasmic reticulum.

Sub G13 F9
~~(TWICE AMENDED)~~
18. The method of Claim 16 wherein said plant cell is further transformed with a second DNA construct according to Claim 9 or 10 and wherein the open reading frame of the DNA sequence from the first DNA construct encodes a different gene than the open reading frame of the second DNA construct.

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19. The method of Claim 18 wherein said pigment is melanin and said proteins are encoded by tyrA and ORF438.

20. The method of Claim 18 wherein said pigment is indigo and said proteins are encoded by tna and pig.

21. The method of Claim 18 wherein said pigment is anthocyanin and said two proteins are the anthocyanin R and C1 proteins.

Sub IT
~~47 (TWICE AMENDED)~~ 40
22. The method of Claim ~~14~~ wherein said fiber tissue is obtained from a cotton burr.

~~30 (TWICE AMENDED)~~
23. A recombinant DNA construct comprising nucleotides 65 – 4163 of SEQ ID NO: 7.

F10
~~31 (TWICE AMENDED)~~
24. A recombinant DNA construct comprising SEQ ID NO: 15.

~~24 (TWICE AMENDED)~~
25. An isolated DNA sequence comprising the sequence shown in SEQ ID NO: 1.

~~25 (TWICE AMENDED)~~
26. An isolated DNA sequence comprising the sequence shown in SEQ ID NO: 12.

F11
~~9 (TWICE AMENDED)~~
28. The DNA sequence according to Claim 1, wherein said transcriptional initiation region is obtained by probing a genomic library derived from a plant fiber tissue.

F12
~~19 (AMENDED)~~ 18
30. The DNA sequence according to Claim ~~59~~, further comprising a sequence encoding a transit peptide from a plant nuclear-encoded gene.

F13
~~20 (AMENDED)~~ 19
31. The DNA sequence according to Claim ~~30~~, wherein said transit peptide is a plastid transit peptide.

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X

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F14

~~21~~ <sup>TWICE
(AMENDED)</sup>

~~18~~

32. The DNA sequence according to Claim ~~59~~, further comprising a sequence encoding a transit peptide which provides for transport across the rough endoplasmic reticulum.

F15

~~22~~ ^(AMENDED)

~~21~~

33. The DNA sequence according to Claim ~~32~~, wherein said sequence further comprises, 3' to said open reading frame, a sequence encoding a vacuolar targeting signal.

34. The DNA sequence of Claim 57 wherein said open reading frame is from a bacterial gene.

35. The DNA sequence of Claim 34 wherein said bacterial gene is selected from the group consisting of ORF438, tyrA, pig and tna.

F16 ~~Sub
Glo~~

~~21~~ <sup>TWICE
(AMENDED)</sup>

36. A DNA construct comprising the DNA sequence of Claim 59.

37. The DNA construct of Claim 36 wherein said cotton plant cell is a cotton fiber cell.

38. A plant cell comprising the DNA construct of Claim 36.

39. A plant comprising the plant cell of Claim 38.

~~23~~ ^(THREE TIMES AMENDED)

~~18~~

42. The DNA sequence according to Claim ~~59~~ wherein said transcriptional initiation region is obtained by probing a genomic library derived from a plant fiber tissue.

~~Sub
TS
F19~~

~~(FOUR TIMES AMENDED)~~

44. A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional initiation region functional in a cotton plant cell and an open reading frame encoding an enzyme in a biosynthetic pathway of melanin or indigo, wherein said transcriptional initiation region is selected from the group consisting of:

- a. nucleotides 65-4163 of SEQ ID NO: 7, and
- b. SEQ ID NO: 15.

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11 (AMENDED)

45. The DNA sequence according to Claim 44, further comprising a sequence encoding a transit peptide from a plant nuclear-encoded gene.

12 (AMENDED)

46. The DNA sequence according to Claim 45, wherein said transit peptide is a plastid transit peptide.

F20

Sub C1

(AMENDED)

47. The DNA sequence according to Claim 44, further comprising a sequence encoding a transit peptide which provides for transport across the rough endoplasmic reticulum.

14 (AMENDED)

48. The DNA sequence according to Claim 47, wherein said sequence further comprises, 3' to said open reading frame, a sequence encoding vacuolar targeting signal.

49. The DNA sequence of Claim 44 wherein said open reading frame is from a bacterial gene.

50. The DNA sequence of Claim 49 wherein said bacterial gene is selected from the group consisting of ORF438, tyrA, pig, and tna.

~~Sub T19~~ F21
51. The DNA construct comprising the DNA sequence of Claim 44.

52. The DNA construct of Claim 51 wherein said cotton plant cell is a cotton fiber cell.

~~Sub T10~~ F22
53. A plant cell comprising the DNA construct of Claim 51.

54. A plant comprising the plant cell of Claim 53.

Q5

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~~17 (TWICE AMENDED)~~

F23
55. The DNA sequence according to Claim 44 wherein said transcriptional initiation region is obtained by probing a genomic library derived from a plant fiber tissue.

~~(FOUR TIMES AMENDED)~~

F24
57. A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional initiation region functional in a cotton fiber cell and an open reading frame encoding an enzyme in the biosynthetic pathway of a pigment, wherein said transcriptional initiation region is selected from the group consisting of:

- nucleotides 65-4163 of SEQ ID NO: 7, and
- SEQ ID NO: 15.

~~(THREE TIMES AMENDED)~~

Sab JII
F25
59. A DNA sequence comprising a transcriptional initiation region functional in a cotton plant cell, wherein said transcriptional initiation region is selected from the group consisting of:

- nucleotides 65-4163 of SEQ ID NO: 7, and
- SEQ ID NO: 15.

~~(AMENDED)~~

F26
61. A recombinant DNA construct comprising nucleotides 57 – 4155 of SEQ ID NO: 11.

~~2 4 (AMENDED)~~

F27
65. An isolated DNA sequence comprising nucleotides 65 – 4163 of SEQ ID NO: 7.

~~2 1 (AMENDED)~~

66. An isolated DNA sequence comprising SEQ ID NO: 15.

F28
67. An isolated nucleic acid sequence comprising a polynucleotide sequence encoding the polypeptide sequence set forth in SEQ ID NO: 2.

68. An isolated nucleic acid sequence comprising a polynucleotide sequence encoding the polypeptide sequence set forth in SEQ ID NO: 13.